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ALIGNMENTS

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GBBB	Interpro; IPROO pfam; pF00713; PRINTS; PR00777 ProDom; PD00421 Serine protease STGNAL.	Eur. J. Bioc -!- FUNCTION INHIBITO THROMBII -!- SIMILAR: EMBL; X7278	SEQUENCE FROSEQUENCE FROMEDLINE=9328 Scacheri E Scacheri E Sawyer R.T "Novel hirucacid sequence	Him2. Hirudinaria mani Eukaryota; Metaz Eukaryota; Metaz Arynchobdellida; NCBI_TaxID=6419;	01-NOV-1998 01-NOV-1998 01-JUN-2001 Hirudin HM2	LT 1 57 Q07557
21 84 26 34 36 48 42 57 84 AA; 9004 MW;	000429; Hirudi 000429; Hirudin; 1. ; Hirudin; 1. 77; HIRUDIN. 7216; Hirudin; se inhibitor;	J. Biochem. 214.295-304(1993) FUNCTION: HIRUDIN IS A POTEN' INHIBITOR. IT FORMS A STABLE THROMBIN, THEREBY ABOLISHING SIMILARITY: BELONGS TO THE H: ; X72786; CAA51293.1; -,	SEQUENCE FROM N.A., AND SEQUENCE MEDLINE=93285156; PubMed=7685281; Scacheri E., Nitti G., Valsasina Sawyer R.T., Sarmientos P.; The Novel hirudin variants from the acid sequence, cDNA cloning and g	HM2. Hirudinaria manillensis (Buffalo leech). Eukaryota; Metazoa; Annelida; Clitellata; Arynchobdellida; Hirudiniformes; Hirudinio NCBL_TaxID-6419;	(TrEMBLrel. 08, Creat (TrEMBLrel. 08, Last (TrEMBLrel. 17, Last precursor (Bufrudin).	PRELIMINARY;
HIRUDIN HM2. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY.	lin. 1 Multigene family; Signal.	J. BIOChem. 214:295-304(1993). FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA- THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINGGEN. SIMILARITY: BELONGS TO THE HIRUDIN FAMILY. J. X72786; CAA51293.1;	SEQUENCE FROM N.A., AND SEQUENCE OF 21-84. MEDLINE=93285156; PubMed=7685281; Scacheri E., Nitti G., Valsasina B., Orsini G., Visco C., Ferrera M., Sawyer R.T., Sarmientos P.; Sawyer R.T., Sarmientos P.; "Novel hirudin variants from the leech Hirudinaria manillensis. Amino acid sequence, cDNA cloning and genomic organization.";	HM2. Hirudinaria manillensis (Buffalo leech). Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinaria. MCBI_TaxID-6419;	, Created) , Last sequence update) , Last annotation update) rudin).	PRT; 84 AA.

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PRINTS; PR00777; HIRUDIN.
ProDom; PD004216; Hirudin
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Eur. J. Biochem. 214:295-304(1993).
-I- FUNCTION: HIRUDIN IS A POTENT THROMBIN-SPECIFIC PROTEASE INHIBITOR. IT FORMS A STABLE NON-COVALENT COMPLEX WITH ALPHA-THROMBIN, THEREBY ABOLISHING ITS ABILITY TO CLEAVE FIBRINGEN.
-I- SIMILARITY: BELONGS TO THE HIRUDIN FAMILY.
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EMBL; X72785; CAA51292.1; -.
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Eukaryota; Metazoa; Annelida; Clitellata;
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01-MAY-2000 (TrEMBLrel: 13, Last sequence update)
01-MAY-2000 (TrEMBLrel: 21, Last sanotation update)
01-JUN-2002 (TrEMBLrel: 21, Last annotation update)
Hirudin variant HV1-THROMBIN inhibitor (Fragment).
Hirudinaria manillensis (Buffalo leech).
Eukaryota, Metazoa; Annellda; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirudinaria manillensis (Buffalo leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hiru
Arynchobdellida; Hirudiniformes; Hirudinidae;
NCBI_TaxID=6419;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation of thrombin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9TWX4;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9TWX4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blood Coagul. Fibrinolysis 2:83-89(1991). HSSP; p01050; 1HIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE.
MEDLINE=92126909;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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HSSP; P01050; 1HIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       manillensis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00777; HIRUDIN.
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Pfam; PF00713; Hirudin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ofam; PF00713; Hirudin; 1.
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2596 MW;
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2580 MW;
(Guppy).
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92.0%;
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Pred. No. 8.2e-10;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 138; DB 5;
Pred. No. 4.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                     BC50A99273A9457E CRC64;
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dae; Hirudinaria.
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leech Hirudinaria
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leech Hirudinaria
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RESULT
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                                                         Query Match
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Matches 21
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Best Local S
Matches 19
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InterPro;
                                                                                                                                                                                                                                       Mueller W.E.G., Schatton W., Wimmer W., Bohm "Initiation of an aquaculture of sponges for production of bioactive metabolities in open Mol. Mar. Biol. Biotechnol. 1:569-579(1999). EMBL; Y18100; CAA77026.1;
                                                                                                                                                                                                                                                                                                                                                                                 Suberites domuncula (Spong Eukaryota; Metazoa; Porife Hadromerida; Suberitidae; NCBI_TaxID=55567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    096962;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2002 (TrEMBLrel. 20,
Tetraspanin-CD63 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Verte Actinopterygil; Neopterygil; Teleostel; Eutach Acanthomorpha; Acanthopterygil; Percomorpha; Cyprinodontiformes; Poeciliidae; Poecilia. NCBI_TaxID=8081;
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ProDom; PD186071; 2Fe-2s_bind; 1.
PROSITE; PS00197; 2Fe2S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00559; MOLYBDOPTERIN_EUK; UNKNOWN_1.
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Ben J., Lim T.-M.,
                                                                                                                                           SEQUENCE
                                                                                                                                                                                  PRINTS; PR00259; TMFOUR.
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                     InterPro; IPRO
Pfam; PF00335;
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YTDCTESGQNL--
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AY034103; AAK5
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; IPRO02888; 2Fe-
; IPRO02564; 2Fe-
; IPRO00564; Aldxa
; IPRO05107; CO_d
; IPRO02346; dehy
                                                                                                                                                                                                   IPR000301; Transmem_4.
0335; transmembrane4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002346; dehydrog_molyb.
IPR000572; Euk_Mb_oxred.
IPR001041; Ferredoxin.
                                                                                                                                         248
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                                                             Conservative
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; Ald_Xan_dh_C2; 1.
; CO_deh_flav_C; 1.
; FAD_binding_5; 1.
                                                                                                                                         AA;
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CLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSHNDG---I
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Porifera;
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                                                                              20.18;
                                                                                                                                         26701 MW;
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2Fe2S_ferredoxin.
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pred. No. 2;
7; Mismatches
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                                                         Score 74; DB Pred. No. 0.38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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dehyrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
                                                                            DB 5
                                                                                                                                                                                                                                                                           , Bohm M., Batel R., Files for their sustainable open systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vertebrata; Euteleostomi;
Euteleostei; Neoteleostei;
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                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atherinomorpha;
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                                                                                               Length 248
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                                                         Indels
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RESULT
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Matches 20
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PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 5.
SMART; SM00109; EGF_CA; 17.
SMART; SM00001; EGF_like; 9.
SMART; SM00004; NL; 2.
                    Q9VU80;
Q9VU80;
01-MAY-2000
01-MAY-2000
01-JUN-2001
CG10089 prot
                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                                                                                                                                                                                     PROSITE; PS50088; ANK_REPEAT; 5.
PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE; PS00010; ASX_HYDROXYL; 18.
PROSITE; PS00022; EGF_1; UNKNOWN_28.
PROSITE; PS01186; EGF_2; 22.
PROSITE; PS01187; EGF_CA; 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Halocynthia roretzi (Sea squirt).
Eukaryota; Metazoa; Chordata; Urochordata;
Stolidobranchia; Pyuridae; Halocynthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB001327; BAA25571.1; HSSP; P00740; 1EDM. InterPro; IPR002110; ANK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hori S., Saitoh T., Matsumoto M., Makabe P. Motch homologue from Halocynthia roretzi in the central nervous system during ascid Dev. Genes Evol. 207:371-380(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1998
01-DEC-2001
           CG10089
                                                                                                                                                                                                                   Hydroxylation;
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001881;
InterPro; IPR001438;
InterPro; IPR000800;
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Drosophila
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                                                                                                                      977 TGTHC-ESLQN--LCTGPNICKNGGSCVQTSNTVSCNCLGGYEGT
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                                                                                                                                           2 TYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTG-EGT
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                                                                                                                                                                                                                                                                                                                                                               PF00023; ank; 6.
PF00008; EGF; 32.
PF00066; notch; 3.
                                                                                                                                                                Similarity 20; Conserv
                    protein.
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IPR000742;
 melanogaster
                             (TrEMBLiel.) (TrEMBLiel. (TrEMBLiel.
                                                                                                                                                                                                         2352
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GTREMBLREL.
GTREMBLREL.
                                                                                                                                                                                                                          Calcium-binding; EGF-like domain; Glycoprotein;
                                                                                                                                                                Conservative
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                                                                      PRELIMINARY;
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                                                                                                                                                                                                                   Repeat
                                                                                                                                                                                                         AA;
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EGF-like.
EGF_2.
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07,
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(Fruit fly)
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Last
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Pred. No. 4.3;
4; Mismatches
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Last annotation updat
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retzi is preferentially
ascidian embryogenesis.
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RESULT 9
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ID Q8RP
AC Q8RP
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DT 01-J
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RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
EMBL; AE003537; AAF49810.1;
DR HSSP; 0.16828; IMKP.
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harlis H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bermann B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Burtis N.I., Barsen M., Dugan-Rocha S., Fleischmann W.,
RA Burtis N.I., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.I., Harrey N., Harris M.,
RA Harris N.I., Harrey N., Harris M.,
RA Harris N.I., Harrey N., Harris M.,
RA Harris N.I., Harray N., Harris M.,
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Best Local
Q8RP58 PRELIMINARY;
Q8RP58;
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000340; DS_phosphatase.
InterPro; IPR000387; TYR_phosphatase
Pfam; PF00782; DSPc; 1.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00195; DSPc;
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                                                                                                                                                                                                                                     QNRDICEGN--CSRGEKCPTGADQDVDGVNIGQGEEEDEGEGE 240
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PS50054; TYR_PHOSPHATASE_DUAL; 1.
608 AA; 66963 MW; 71EA135E5C7660D1 CRC64;
                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                  19.3%;
                                                                                                                                                                                                                                                                                                                                             10;
                                                     Created)
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     Last sequence update)
Last annotation updat
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        update)
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Q93NY8;
01-DEC-2001
01-DEC-2001
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                 Major surface protein (Fragment).
Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; alpha subdivision; Ricketts
                                                                                                                                                                     Pfam; PF01617;
                                                                                                                                                                                             J. Clin. Microbiol. 39:2466-2476(2001).
EMBL; AF356509; AAK69699.1; -.
                                                                                                                                                                                                                    combinations of immunoreactive recombinant
                                                                                                                                                                                                                                                      MEDLINE=21320744; PubMed=11427556;
Lodes M.J., Mohamath R., Reynolds L.D., McNeill
Bruinsma E.S., Benson D.R., Hofmeister E., Reed
                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infect. Immun. 70:1230-1234
EMBL; AF443418; AAL77334.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Major surface protein 2 hypervariable region {\tt MSP2}.
                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                            Persing D.H.;
                                                                                                                                                                                                                                                                                             STRAIN-WI
                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                           Anaplasmataceae; Anaplasma.
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245
                                               185
                                                                                                                                                                                                                              Serodiagnosis of human granulocytic ehrlichiosis by using
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                      57
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KDLVQELTPEE 255
                                               CGDNGSSTITTSGTNVSETGQVFRDFIRATLKEDGSKNWPTSSGTGTPKPVTNDNAKAVA 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGDNGSSTITTSGTNVSETGQVFRDFIRATLKEDGSKNWPTSSGTGTPKPVTNDNAKAVA 123
                                                                    CTESGQNLCLCEGSNVCGQGN-----KCILGSDGEKN-QCVTGEGTPKPQSHNDGDF--
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                      ----EEIPEE
                                                                                                         Similarity
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Proteobacteria; alpha subdivision; Rickettsiales;
                                                                                                                                                                                 IPR002566; Surface_
                                                                                                                                              323
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                                                                                               Conservative
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                                                                                                                                              AA;
                                                                                                                                                                   Surface_Ag_2;
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                     62
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                                                                                                                                              34533 MW;
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29.6%;
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Pred. No. 1
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Pred. No. 0.77;
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                                                                                                                                              51E0646ED4F8FDED CRC64;
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1.5;
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                                                                                                                    Length 323
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Matches 21
  Query
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01-FEB-1997
01-DEC-2001
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Q94711;
                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE-92106337; PubMed=1762150;

Nielsen E., You Y., Forney J.;

"Cysteine residue periodicity is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00050; kazal; 1.
SMART; SM00274; FOLN; 1.
SMART; SM00280; KAZAL; 1
SEQUENCE 315 AA; 3581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Gallus gallus (Chicken).
Filterronta: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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FLIK.
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01-DEC-2001
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01-NOV-1999
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                                                                                            variable surface proteins from Paramecium J. Mol. Biol. 222:835-841(1991). EMBL; M65164; AAA61740.1;
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                                    InterPro; IPR002895; Paramecium_SA. Pfam; PF01508; Paramecium_SA; 25. SEQUENCE 2233 AA; 237078 MW; CO
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                                                                                                                                                                                                                                                                                                                   Paramecium tetraurelia.
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                                                                                                                                  Anaplasma
Bacteria;
                 "Multiple p44 genes encoding major outer membrane proteins expressed in the human granulocytic chrlichiosis agent."; J. Biol. Chem. 274:17828-17836(1999).

EMBL; AF135256; AAD41480.1;
                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2002 (TrEMBLrel. 21, 44 kDa major outer membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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01-JUN-2002
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                                                           MEDLINE=99292751; PubMed=10364227; Zhi N., Ohashi N., Rikihisa Y.;
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        InterPro;
                                                                                         SEQUENCE FROM N.A.
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nes 17; Conserv
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                                                                                                                                                                                                                                                                                                                                   CTESGQNLCLCEGSNVCGQGN----KCILGSDGEKN-QCVTGEGTPKPQSHNDGDF--
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21; Conservative
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         IPR002566;
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Proteobacteria;
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184 AA;
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19245 MW;
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EMBL; AF02923; AAC31309.1; -.
InterPro; IPR002566; Surface_Ag_msp4.
Ffam; PF01617; Surface_Ag_2; 1.
SEQUENCE 364 AA; 38806 MW; 32DA9B830A6153F2 CRC64;
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084968;
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-USG3
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anaplasma phagocytophilum (Ehrlichia phagocytophila).
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Anaplasmataceae; Anaplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TIEMBLIEL. 08, Created)
01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-JUN-2002 (TIEMBLIEL. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98339872; PubMed=9673253;
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Major surface protein-2C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 KDLVQELTPEE 190
                                                            286 KDLVQELTPEE 296
                                                                                                                       226 CGDNGSSTITNSGANVSETGQVFRDFIRATLKEDGSKNWPTSSGTGTPKPVTNDNAKAVA 285
                                                                                                                                                                                              Match 18.5%;
Local Similarity 29.6%;
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                                                                                        57 -----EEIPEE 62
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278 AA;
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29389 MW;
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              2002, 16:17:37
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